



SEQUENCE LISTING

(1) GENERAL INFORMATION:

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(i) APPLICANT: Choi, Yongwon  
Wong, Brian  
Josien, Regis  
Steinman, Ralph

(ii) TITLE OF INVENTION: A PROTEIN BELONGING TO THE TNF SUPERFAMILY INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC ACIDS ENCODING SAME, AND METHODS OF USE THEREOF

(iii) NUMBER OF SEQUENCES: 18

(iv) CORRESPONDENCE ADDRESS:

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(C) CITY: Hackensack  
(D) STATE: New Jersey  
(E) COUNTRY: USA  
(F) ZIP: 07601

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US  
(B) FILING DATE:  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Jackson Esq., David A.  
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(C) REFERENCE/DOCKET NUMBER: 600-1-200 CIP N

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1823 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAG ATG GAT CCT AAT AGA ATA TCA GAA GAT GGC ACT CAC TGC ATT TAT  
48

Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Gly Thr His Cys Ile Tyr  
1 5 10 15

AGA ATT TTG AGA CTC CAT GAA AAT GCA GAT TTT CAA GAC ACA ACT CTG  
96

Arg Ile Leu Arg Leu His Glu Asn Ala Asp Phe Gln Asp Thr Thr Leu  
20 25 30

GAG AGT CAA GAT ACA AAA TTA ATA CCT GAT TCA TGT AGG AGA ATT AAA  
144

Glu Ser Gln Asp Thr Lys Leu Ile Pro Asp Ser Cys Arg Arg Ile Lys  
35 40 45

CAG GCC TTT CAA GGA GCT GTG CAA AAG GAA TTA CAA CAT ATC GTT GGA  
192

Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val Gly  
50 55 60

TCA CAG CAC ATC AGA GCA GAG AAA GCG ATG GTG GAT GGC TCA TGG TTA  
240

Ser Gln His Ile Arg Ala Glu Lys Ala Met Val Asp Gly Ser Trp Leu  
65 70 75 80

CO  
OFFICE

GAT CTG GCC AAG AGG AGC AAG CTT GAA GCT CAG CCT TTT GCT CAT CTC  
288

Asp Leu Ala Lys Arg Ser Lys Leu Glu Ala Gln Pro Phe Ala His Leu  
85 90 95

ACT ATT AAT GCC ACC GAC ATC CCA TCT GGT TCC CAT AAA GTG AGT CTG  
336

Thr Ile Asn Ala Thr Asp Ile Pro Ser Gly Ser His Lys Val Ser Leu  
100 105 110

TCC TCT TGG TAC CAT GAT CGG GGG TGG GGT AAG ATC TCC AAC ATG ACT  
384

Ser Ser Trp Tyr His Asp Arg Gly Trp Gly Lys Ile Ser Asn Met Thr  
115 120 125

TTT AGC AAT GGA AAA CTA ATA GTT AAT CAG GAT GGC TTT TAT TAC CTG  
432

Phe Ser Asn Gly Lys Leu Ile Val Asn Gln Asp Gly Phe Tyr Tyr Leu  
130 135 140

TAT GCC AAC ATT TGC TTT CGA CAT CAT GAA ACT TCA GGA GAC CTA GCT  
480

Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Asp Leu Ala  
145 150 155 160

ACA GAG TAT CTT CAA CTA ATG GTG TAC GTC ACT AAA ACC AGC ATC AAA  
528

Thr Glu Tyr Leu Gln Leu Met Val Tyr Val Thr Lys Thr Ser Ile Lys  
165 170 175

ATC CCA AGT TCT CAT ACC CTG ATG AAA GGA GGA AGC ACC AAG TAT TGG  
576

Ile Pro Ser Ser His Thr Leu Met Lys Gly Gly Ser Thr Lys Tyr Trp  
180 185 190

TCA GGG AAT TCT GAA TTC CAT TTT TAT TCC ATA AAC GTT GGT GGA TTT  
624

Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe  
195 200 205

TTT AAG TTA CGG TCT GGA GAG GAA ATC AGC ATC GAG GTC TCC AAC CCC  
672

Phe Lys Leu Arg Ser Gly Glu Glu Ile Ser Ile Glu Val Ser Asn Pro  
210 215 220

TCC TTA CTG GAT CCG GAT CAG GAT GCA ACA TAC TTT GGG GCT TTT AAA

720

Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys

225            230            235            240

GTT CGA GAT ATA GAT TGA GCCCCAGTTT TTGGAGTGTT ATGTATTTC

768

Val Arg Asp Ile Asp \*

245

TGGATGTTTG GAAACATTTT TTAACAACAG CCAAGAAAGA TGTATATAGG

TGTGTGAGAC 828

TACTAAGAGG CATGGCCCAA CGGTACACGA CTCAGTATCC ATGCTCTTGA

CCTTGTAAG 888

AACACGCGTA TTTACAGCCA GTGGGAGATG TTAGACTCAT GGTGTGTTAC

ACAATGGTTT 948

TTAAATTTTG TAATGAATTC CTAGAATTAA ACCAGATTGG AGCAATTACG

GGTTGACCTT 1008

ATGAGAAACT GCATGTGGGC TATGGGAGGG GTTGGTCCCT GGTCATGTGC

CCCTTCGCAG 1068

CTGAAGTGA GAGGGTGTC TCTAGCGCAA TTGAAGGATC ATCTGAAGGG

GCAAATTCTT 1128

TTGAATTGTT ACATCATGCT GGAACCTGCA AAAAATACTT TTTCTAATGA

GGAGAGAAAA 1188

TATATGTATT TTTATATAAT ATCTAAAGTT ATATTTTCAGA TGTAAATGTTT

TCTTTGCAAA 1248

GTATTGTAAA TTATATTTGT GCTATAGTAT TTGATTCAAA ATATTTAAAA

ATGTCTTGCT 1308

GTTGACATAT TTAATGTTTT AAATGTACAG ACATATTTAA CTGGTGCACT

TTGTAAATTC 1368

CCTGGGGAAA ACTTGCAGCT AAGGAGGGGA AAAAATGTTG TTTCTAATA

TCAAATGCAG 1428

TATATTTCTT CGTTCTTTTT AAGTTAATAG ATTTTTTCAG ACTTGTCAG

CCTGTGCAAA 1488

AAAATTAAAA TGGATGCCTT GAATAATAAG CAGGATGTTG GCCACCAGGT

GCCTTTCAAA 1548

TTAGAAACT AATTGACTTT AGAAAGCTGA CATTGCCAAA AAGGATACAT  
AATGGGCCAC 1608

TGAAATCTGT CAAGAGTAGT TATATAATTG TTGAACAGGT GTTTTCCAC  
AAGTGCCGCA 1668

AATTGTACCT TTTTTGTTT TTTTCAAAT AGAAAAGTTA TTAGTGGTTT  
ATCAGCAAAA 1728

AAGTCCAATT TTAATTTAGT AAATGTTATC TTATACTGTA CAATAAAAAC  
ATTGCCTTTG 1788

AATGTTAATT TTTTGGTACA AAAGTCGACG GCCGC 1823

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 246 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Gly Thr His Cys Ile Tyr  
1 5 10 15

Arg Ile Leu Arg Leu His Glu Asn Ala Asp Phe Gln Asp Thr Thr Leu  
20 25 30

Glu Ser Gln Asp Thr Lys Leu Ile Pro Asp Ser Cys Arg Arg Ile Lys  
35 40 45

Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val Gly  
50 55 60

Ser Gln His Ile Arg Ala Glu Lys Ala Met Val Asp Gly Ser Trp Leu  
65 70 75 80

Asp Leu Ala Lys Arg Ser Lys Leu Glu Ala Gln Pro Phe Ala His Leu  
85 90 95

Thr Ile Asn Ala Thr Asp Ile Pro Ser Gly Ser His Lys Val Ser Leu  
100 105 110

Ser Ser Trp Tyr His Asp Arg Gly Trp Gly Lys Ile Ser Asn Met Thr  
115 120 125

Phe Ser Asn Gly Lys Leu Ile Val Asn Gln Asp Gly Phe Tyr Tyr Leu  
130 135 140

Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Asp Leu Ala  
145 150 155 160

Thr Glu Tyr Leu Gln Leu Met Val Tyr Val Thr Lys Thr Ser Ile Lys  
165 170 175

Ile Pro Ser Ser His Thr Leu Met Lys Gly Gly Ser Thr Lys Tyr Trp  
180 185 190

Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe  
195 200 205

Phe Lys Leu Arg Ser Gly Glu Glu Ile Ser Ile Glu Val Ser Asn Pro  
210 215 220

Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys  
225 230 235 240

Val Arg Asp Ile Asp \*  
245

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2237 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mus musculus

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 142..1092

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCCACGTCCC GGGGAGCCAC TGCCAGGACC TTTGTGAACC GGTCGGGGCG  
GGGGCCGTGG 60

CGGAGTCTGC TCGGCGGTGG GTGGCCCGAG AAGGGAGAGA ACGATCGCGG  
AGCAGGGCGC 120

CCGAACTCCG GGCGCCGCGC C ATG CGC CGG GCC AGC CGA GAC TAC GGC AAG  
171

Met Arg Arg Ala Ser Arg Asp Tyr Gly Lys  
250 255

TAC CTG CGC AGC TCG GAA GAG ATG GGC AGC GGC CCC GGC GTC CCA CAC  
219

Tyr Leu Arg Ser Ser Glu Glu Met Gly Ser Gly Pro Gly Val Pro His  
260 265 270

GAA GGT CCG CTG CAC CCC GCG CCT TCT GCA CCG GCT CCG GCG CCG CCA  
267

Glu Gly Pro Leu His Pro Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro  
275 280 285

CCC GCC GCC TCC CGC TCC ATG TTC CTG GCC CTC CTG GGG CTG GGA CTG  
315

Pro Ala Ala Ser Arg Ser Met Phe Leu Ala Leu Leu Gly Leu Gly Leu  
290 295 300

GGC CAG GTG GTC TGC AGC ATC GCT CTG TTC CTG TAC TTT CGA GCG CAG  
363

Gly Gln Val Val Cys Ser Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln  
305 310 315 320

ATG GAT CCT AAC AGA ATA TCA GAA GAC AGC ACT CAC TGC TTT TAT AGA  
411

Met Asp Pro Asn Arg Ile Ser Glu Asp Ser Thr His Cys Phe Tyr Arg  
325 330 335

ATC CTG AGA CTC CAT GAA AAC GCA GGT TTG CAG GAC TCG ACT CTG GAG  
459

Ile Leu Arg Leu His Glu Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu  
340 345 350

AGT GAA GAC ACA CTA CCT GAC TCC TGC AGG AGG ATG AAA CAA GCC TTT  
507

Ser Glu Asp Thr Leu Pro Asp Ser Cys Arg Arg Met Lys Gln Ala Phe  
355 360 365

CAG GGG GCC GTG CAG AAG GAA CTG CAA CAC ATT GTG GGG CCA CAG CGC  
555

Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val Gly Pro Gln Arg  
370 375 380

TTC TCA GGA GCT CCA GCT ATG ATG GAA GGC TCA TGG TTG GAT GTG GCC  
603

Phe Ser Gly Ala Pro Ala Met Met Glu Gly Ser Trp Leu Asp Val Ala  
385 390 395 400

CAG CGA GGC AAG CCT GAG GCC CAG CCA TTT GCA CAC CTC ACC ATC AAT  
651

Gln Arg Gly Lys Pro Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn  
405 410 415

GCT GCC AGC ATC CCA TCG GGT TCC CAT AAA GTC ACT CTG TCC TCT TGG  
699

Ala Ala Ser Ile Pro Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp  
420 425 430

TAC CAC GAT CGA GGC TGG GCC AAG ATC TCT AAC ATG ACG TTA AGC AAC  
747

Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn  
435 440 445

GGA AAA CTA AGG GTT AAC CAA GAT GGC TTC TAT TAC CTG TAC GCC AAC  
795

Gly Lys Leu Arg Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn  
450 455 460

ATT TGC TTT CGG CAT CAT GAA ACA TCG GGA AGC GTA CCT ACA GAC TAT  
843

Ile Cys Phe Arg His His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr  
465 470 475 480

CTT CAG CTG ATG GTG TAT GTC GTT AAA ACC AGC ATC AAA ATC CCA AGT  
891

Leu Gln Leu Met Val Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser  
485 490 495

TCT CAT AAC CTG ATG AAA GGA GGG AGC ACG AAA AAC TGG TCG GGC AAT



939

Ser His Asn Leu Met Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn  
500 505 510

TCT GAA TTC CAC TTT TAT TCC ATA AAT GTT GGG GGA TTT TTC AAG CTC 987  
Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu  
515 520 525

CGA GCT GGT GAA GAA ATT AGC ATT CAG GTG TCC AAC CCT TCC CTG CTG  
1035  
Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu  
530 535 540

GAT CCG GAT CAA GAT GCG ACG TAC TTT GGG GCT TTC AAA GTT CAG GAC  
1083  
Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp  
545 550 555 560

ATA GAC TGA GACTCATTTC GTGGAACATT AGCATGGATG TCCTAGATGT  
1132  
Ile Asp \*

TTGGAAACTT CTTAAAAAAT GGATGATGTC TATACATGTG TAAGACTACT  
AAGAGACATG 1192

GCCCACGGTG TATGAAACTC ACAGCCCTCT CTCTTGAGCC CTGTACAGGT  
TGTGTATATG 1252

TAAAGTCCAT AGGTGATGTT AGATTCATGG TGATTACACA ACGGTTTTAC  
AATTTTGTAA 1312

TGATTTCTTA GAATTGAACC AGATTGGGAG AGGTATTCCG ATGCTTATGA  
AAAACCTTACA 1372

CGTGAGCTAT GGAAGGGGGT CACAGTCTCT GGTCTAACCC CTGGACATGT  
GCCACTGAGA 1432

ACCTTGAAAT TAAGAGGATG CCATGTCATT GCATAGAAAT GATAGTGTGA  
AGGGTTAAGT 1492

TCTTTTGAAT TGTTACATTG CGCTGGGACC TGCAAATAAG TTCTTTTTTT  
CTAATGAGGA 1552

GAAAAATATA TGTATTTTAA TATAATGTCT AAAGTTATAT TTCAGGTGTA  
ATGTTTTCTG 1612

TGCAAAGTTT TGTA AATTAT ATTTGTGCTA TAGTATTTGA TTCAA AATAT  
TTAAAAATGT 1672

CTCACTGTTG ACATATTTAA TGTTTTAAAT GTACAGATGT ATTAACTGG  
TGCAC TTTGT 1732

AATTCCCCTG AAGGTACTCG TAGCTAAGGG GGCAGAATAC TGTTTCTGGT  
GACCACATGT 1792

AGTTTATTTT TTTATTTCTTT TTA ACTTAAT AGAGTCTTCA GACTTG TCAA  
AACTATGCAA 1852

GCAAAATAAA TAAATAAAAA TAAAATGAAT ACCTTGAATA ATAAGTAGGA  
TGTTGGTCAC 1912

CAGGTGCCTT TCAAATTTAG AAGCTAATTG ACTTTAGGAG CTGACATAGC  
CAAAAAGGAA 1972

CATAATAGGC TACTGAAATC TGTCAGGAGT ATTTATGCAA TTATTGAACA  
GGTGTCTTTT 2032

TTTACAAGAG CTACAAATTG TAAATTTTGG TTTCTTTTTT TTCCCATAGA  
AAATGTACTA 2092

TAGTTTATCA GCCAAAAAAC AATCCACTTT TTAATTTAGT GAAAGTTATT  
TTATTATACT 2152

GTACAATAAA AGCATTGTCT CTGAATGTTA ATTTTTTGGT ACAAAAAATA  
AATTTGTACG 2212

AAAAAAAAAA AAAAAAAAAA AAAAA

2237

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Arg Arg Ala Ser Arg Asp Tyr Gly Lys Tyr Leu Arg Ser Ser Glu

1

5

10

15

Glu Met Gly Ser Gly Pro Gly Val Pro His Glu Gly Pro Leu His Pro  
20 25 30

Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser  
35 40 45

Met Phe Leu Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser  
50 55 60

Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile  
65 70 75 80

Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu  
85 90 95

Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro  
100 105 110

Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys  
115 120 125

Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala  
130 135 140

Met Met Glu Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys Pro Glu  
145 150 155 160

Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser  
165 170 175

Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp  
180 185 190

Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn  
195 200 205

Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His  
210 215 220

Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr  
225 230 235 240

Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys  
245 250 255

Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr

260	265	270
Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile		
275	280	285
Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala		
290	295	300
Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp *		
305	310	315

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mus musculus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Gln	Gln	Pro	Met	Asn	Tyr	Pro	Cys	Pro	Gln	Ile	Phe	Trp	Val	Asp
1		5		10		15									

Ser	Ser	Ala	Thr	Ser	Ser	Trp	Ala	Pro	Pro	Gly	Ser	Val	Phe	Pro	Cys
	20			25				30							

Pro	Ser	Cys	Gly	Pro	Arg	Gly	Pro	Asp	Gln	Arg	Arg	Pro	Pro	Pro	Pro
	35			40				45							

Pro	Pro	Pro	Val	Ser	Pro	Leu	Pro	Pro	Pro	Ser	Gln	Pro	Leu	Pro	Leu
	50			55				60							

Pro	Pro	Leu	Thr	Pro	Leu	Lys	Lys	Lys	Asp	His	Asn	Thr	Asn	Leu	Trp
	65			70			75		80						

Leu Pro Val Val Phe Phe Met Val Leu Val Ala Leu Val Gly Met Gly

85	90	95
Leu Gly Met Tyr Gln Leu Phe His Leu Gln Lys Glu Leu Ala Glu Leu		
100	105	110
Arg Glu Phe Thr Asn Gln Ser Leu Lys Val Ser Ser Phe Glu Lys Gln		
115	120	125
Ile Ala Asn Pro Ser Thr Pro Ser Glu Lys Lys Glu Pro Arg Ser Val		
130	135	140
Ala His Leu Thr Gly Asn Pro His Ser Arg Ser Ile Pro Leu Glu Trp		
145	150	155 160
Glu Asp Thr Tyr Gly Thr Ala Leu Ile Ser Gly Val Lys Tyr Lys Lys		
165	170	175
Gly Gly Leu Val Ile Asn Glu Thr Gly Leu Tyr Phe Val Tyr Ser Lys		
180	185	190
Val Tyr Phe Arg Gly Gln Ser Cys Asn Asn Gln Pro Leu Asn His Lys		
195	200	205
Val Tyr Met Arg Asn Ser Lys Tyr Pro Glu Asp Leu Val Leu Met Glu		
210	215	220
Glu Lys Arg Leu Asn Tyr Cys Thr Thr Gly Gln Ile Trp Ala His Ser		
225	230	235 240
Ser Tyr Leu Gly Ala Val Phe Asn Leu Thr Ser Ala Asp His Leu Tyr		
245	250	255
Val Asn Ile Ser Gln Leu Ser Leu Ile Asn Phe Glu Glu Ser Lys Thr		
260	265	270
Phe Phe Gly Leu Tyr Lys Leu		
275		

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mus musculus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Pro Ser Ser Gly Ala Leu Lys Asp Leu Ser Phe Ser Gln His Phe  
1            5            10            15

Arg Met Met Val Ile Cys Ile Val Leu Leu Gln Val Leu Leu Gln Ala  
20            25            30

Val Ser Val Ala Val Thr Tyr Met Tyr Phe Thr Asn Glu Met Lys Gln  
35            40            45

Leu Gln Asp Asn Tyr Ser Lys Ile Gly Leu Ala Cys Phe Ser Lys Thr  
50            55            60

Asp Glu Asp Phe Trp Asp Ser Thr Asp Gly Glu Ile Leu Asn Arg Pro  
65            70            75            80

Cys Leu Gln Val Lys Arg Gln Leu Tyr Gln Leu Ile Glu Glu Val Thr  
85            90            95

Leu Arg Thr Phe Gln Asp Thr Ile Ser Thr Val Pro Glu Lys Gln Leu  
100            105            110

Ser Thr Pro Pro Leu Pro Arg Gly Gly Arg Pro Gln Lys Val Ala Ala  
115            120            125

His Ile Thr Gly Ile Thr Arg Arg Ser Asn Ser Ala Leu Ile Pro Ile  
130            135            140

Ser Lys Asp Gly Lys Thr Leu Gly Gln Lys Ile Glu Ser Trp Glu Ser  
145            150            155            160

Ser Arg Lys Gly His Ser Phe Leu Asn His Val Leu Phe Arg Asn Gly  
165            170            175

Glu Leu Val Ile Glu Gln Glu Gly Leu Tyr Tyr Ile Tyr Ser Gln Thr  
180            185            190

Tyr Phe Arg Phe Gln Glu Ala Glu Asp Ala Ser Lys Met Val Ser Lys  
195 200 205

Asp Lys Val Arg Thr Lys Gln Leu Val Gln Tyr Ile Tyr Lys Tyr Thr  
210 215 220

Ser Tyr Pro Asp Pro Ile Val Leu Met Lys Ser Ala Arg Asn Ser Cys  
225 230 235 240

Trp Ser Arg Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly  
245 250 255

Leu Phe Glu Leu Lys Lys Asn Asp Arg Ile Phe Val Ser Val Thr Asn  
260 265 270

Glu His Leu Met Asp Leu Asp Gln Glu Ala Ser Phe Phe Gly Ala Phe  
275 280 285

Leu Ile Asn  
290

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mus musculus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Gly Thr Arg Gly Leu Gln Gly Leu Gly Gly Arg Pro Gln Gly Arg  
1 5 10 15

Gly Cys Leu Leu Leu Ala Val Ala Gly Ala Thr Ser Leu Val Thr Leu  
20 25 30

Leu Leu Ala Val Pro Ile Thr Val Leu Ala Val Leu Ala Leu Val Pro  
35 40 45

Gln Asp Gln Gly Arg Arg Val Glu Lys Ile Ile Gly Ser Gly Ala Gln  
50 55 60

Ala Gln Lys Arg Leu Asp Asp Ser Lys Pro Ser Cys Ile Leu Pro Ser  
65 70 75 80

Pro Ser Ser Leu Ser Glu Thr Pro Asp Pro Arg Leu His Pro Gln Arg  
85 90 95

Ser Asn Ala Ser Arg Asn Leu Ala Ser Thr Ser Gln Gly Pro Val Ala  
100 105 110

Gln Ser Ser Arg Glu Ala Ser Ala Trp Met Thr Ile Leu Ser Pro Ala  
115 120 125

Ala Asp Ser Thr Pro Asp Pro Gly Val Gln Gln Leu Pro Lys Gly Glu  
130 135 140

Pro Glu Thr Asp Leu Asn Pro Glu Leu Pro Ala Ala His Leu Ile Gly  
145 150 155 160

Ala Trp Met Ser Gly Gln Gly Leu Ser Trp Glu Ala Ser Gln Glu Glu  
165 170 175

Ala Phe Leu Arg Ser Gly Ala Gln Phe Ser Pro Thr His Gly Leu Ala  
180 185 190

Leu Pro Gln Asp Gly Val Tyr Tyr Leu Tyr Cys His Val Gly Tyr Arg  
195 200 205

Gly Arg Thr Pro Pro Ala Gly Arg Ser Arg Ala Arg Ser Leu Thr Leu  
210 215 220

Arg Ser Ala Leu Tyr Arg Ala Gly Gly Ala Tyr Gly Arg Gly Ser Pro  
225 230 235 240

Glu Leu Leu Leu Glu Gly Ala Glu Thr Val Thr Pro Val Val Asp Pro  
245 250 255

Ile Gly Tyr Gly Ser Leu Trp Tyr Thr Ser Val Gly Phe Gly Gly Leu  
260 265 270

Ala Gln Leu Arg Ser Gly Glu Arg Val Tyr Val Asn Ile Ser His Pro



275	280	285	
Asp Met Val Asp Tyr Arg Arg Gly Lys Thr Phe Phe Gly Ala Val Met			
290	295	300	
Val Gly			
305			

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mus musculus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ser Thr Glu Ser Met Ile Arg Asp Val Glu Leu Ala Glu Glu Ala			
1	5	10	15
Leu Pro Gln Lys Met Gly Gly Phe Gln Asn Ser Arg Arg Cys Leu Cys			
20	25	30	
Leu Ser Leu Phe Ser Phe Leu Leu Val Ala Gly Ala Thr Thr Leu Phe			
35	40	45	
Cys Leu Leu Asn Phe Gly Val Ile Gly Pro Gln Arg Asp Glu Lys Phe			
50	55	60	
Pro Asn Gly Leu Pro Leu Ile Ser Ser Met Ala Gln Thr Leu Thr Leu			
65	70	75	80
Arg Ser Ser Ser Gln Asn Ser Ser Asp Lys Pro Val Ala His Val Val			
85	90	95	
Ala Asn His Gln Val Glu Glu Gln Leu Glu Trp Leu Ser Gln Arg Ala			

100	105	110
Asn Ala Leu Leu Ala Asn Gly Met Asp Leu Lys Asp Asn Gln Leu Val		
115	120	125
Val Pro Ala Asp Gly Leu Tyr Leu Val Tyr Ser Gln Val Leu Phe Lys		
130	135	140
Gly Gln Gly Cys Pro Asp Tyr Val Leu Leu Thr His Thr Val Ser Arg		
145	150	155
		160
Phe Ala Ile Ser Tyr Gln Glu Lys Val Asn Leu Leu Ser Ala Val Lys		
165	170	175
Ser Pro Cys Pro Lys Asp Thr Pro Glu Gly Ala Glu Leu Lys Pro Trp		
180	185	190
Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp		
195	200	205
Gln Leu Ser Ala Glu Val Asn Leu Pro Lys Tyr Leu Asp Phe Ala Glu		
210	215	220
Ser Gly Gln Val Tyr Phe Gly Val Ile Ala Leu		
225	230	235

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "PRIMER"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGAAGATCC TGACCGAGCG

20

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "PRIMER"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TACTTGCGCT GAGGAGGAGC

20

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "PRIMER"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCTGAGACTC CATGAAAACG C

21

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "PRIMER"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TAACCCTTAG TTTCCGTTG C

21

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "PRIMER"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ACCCAGATGG ACTTCTGTGG

20

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "PRIMER"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TTTCCTTCGA CGTGCTAACG

20

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GTAATGATCA GTCAACGGGG GAC

23

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCAGCAAGCT TGCAACCTTA ACCA

24

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTGGCAACTG GACTTCCAGC G

21

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GCGTTGACTC GAAGGCTCCC G

21